Amendments to the Claims:

This listing of claims will replace all prior versions and listings of claims in the application.

Listing of Claims:

1. Cancelled
2. Cancelled
3. Cancelled.
4. Cancelled
5. Cancelled
6. Cancelled
7. Cancelled
8. Cancelled
9. Cancelled
10. Cancelled
11. Cancelled
12. (Currently Amended) A high-throughput method for assaying for changes in protein-protein interactions in response to ~~intracellular or extracellular factors or~~ a test agent comprising:
    (a) introducing one or more prey proteins in cells, wherein [[a]] the prey proteins ~~is~~ are labelled with an epitope tag permitting separation of the prey proteins from other proteins in the cells and wherein the prey proteins can interact with a SMURF to form protein-protein interactions which define a network of interactions involved in signal transduction pathways regulated by a SMURF;
    (b) introducing one or more bait protein in the cells, wherein the bait protein is a SMURF ~~a bait protein is~~ labelled with a detectable substance permitting identification of the bait protein and protein-protein interactions comprising a prey protein and the bait protein;
    (c) inducing formation of the protein-protein interactions ~~between a prey proteins and bait proteins~~ in the presence of the test agent;

(d) ~~introducing an intracellular or extracellular factor or test agent; (e)~~ assaying in a high-throughput format the protein-protein interactions ~~comprising a prey protein and bait protein~~; and ~~(f)~~ (e) comparing the assayed protein-protein interactions with protein-protein interactions assayed in the absence of the ~~intracellular or extracellular factor~~ test agent.

13. Cancelled

14. (Previously presented) A method of claim 12 wherein an increase in the protein-protein interactions with a test agent indicates that the agent is an agonist of the interaction and a decrease in the amount of protein-protein interactions indicates that the agent is an antagonist.

15. (Currently Amended) A method of claim [[5]] 12 wherein the cells are mammalian cells.

16. Cancelled

17. Cancelled

18. Cancelled

19. (Currently Amended) A method as claimed in claim [[5]] 12 wherein the detectable substance is an enzyme, radioisotope, fluorescent label, luminescent label, or an enzymatic label.

20. (Previously presented) A method of claim 19 wherein the detectable substance is an enzymatic label.

21. (Currently amended) A method of claim 20 wherein the detectable substance is luciferase~~, in particular Renilla luciferase~~.

22. (Currently Amended) A method as claimed in claim 12 [[17]] wherein two or more prey proteins are introduced into the cells.

23. (Currently Amended) A method of claim 12 [[17]] wherein the epitope tag is FLAG, hemagglutinin, His6, or an Ig sequence.

24. (Currently Amended) A method of claim [[5]] 12 wherein the prey protein comprises a protein sequence obtained from genomic DNA sequences or random sequences.

25. (Currently Amended) A method of claim [[5]] 12 wherein the prey protein comprises a library of protein sequences.

26. Cancelled

27. Cancelled

28. Cancelled

29. Cancelled

30. Cancelled

31. Cancelled

32. (New) A method of claim 12 wherein in step (e) the protein-protein interactions are compared using a matix comprising a color gradient displaying the magnitude of the protein-protein interactions.

33. (New) A method of claim 32 wherein the matrix comprises 100 by 100 protein-protein interactions.

34. (New) A method of claim 32 wherein in step (e) the types, quantities or kinds of protein-protein interactions are compared.

35. (New) A method of claim 12 wherein in step (c) the protein-protein interactions are induced by introducing an intracellular or extracellular signal.

36. (New) A method of claim 12 wherein steps (a) to (e) are performed using an integrated modular system.

37. (New) A method of claim 12 wherein step (d) further comprises purifying proteins of the protein-protein interactions in an automated immunoprecipitation module, preparing fragments of the proteins suitable for mass spectrometry in an analysis module; and analyzing the fragments in a mass spectrometer module.